DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

Attorney Docket No. 5470-338

As a below named inventor, I hereby declare that:

the specification of which

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled REGULATION OF QUINOLATE PHOSPHORIBOSYL TRANSFERASE EXPRESSION,

is attached hereto	
OR	
was filed on 10 February 1998 as United States Application No. 09/021,2	286.
I hereby state that I have reviewed and understand the contents of the above-specification, including the claims, as amended by any amendment referred to	

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37 Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States of America, listed below and have also identified below any foreign application for patent or inventor's certificate, or of any PCT International application having a filing date before that of the application on which priority is claimed.

NONE			Yes No
Number	Country	MM/DD/YYYY Filed .	Priority Claimed

I hereby claim the benefit under Title 35, United States Code, § 119(e) of any United States provisional application(s) listed below.

60/049,471	June 12, 1997
Application Number(s)	Filing Date (MM/DD/YYYY)

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) or § 365(c) of any PCT international application designating the United States

of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application(s) in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application (37 C.F.R. § 1.63(d)).

None		
Appln. Serial No.	Filing Date	Status Patented/Pending/Abandoned

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following registered attorney(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Full name of first inventor: N	Mark A.	Conkling
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Inventor's Signature: 2

1/2/6 Date: 5/12/98

Residence:

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Citizenship:

United States of America

Full name of second	ond inventor: W	Ven Song				
Inventor's Signature:	Wender	Date: _	5/12/98			
Oignature.			No. C. 9			
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Full name of third inventor:

Nandini Mendu

Inventor's

Signature: Nandini Me

Date: May 13

Residence:

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Durham, North Carolina 27707

Citizenship:

India

(A) NAME/KEY: CDS
(B) LOCATION: 52..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

(X1) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
CAAAAACTAT TTTCCACAAA ATTCATTTCA CAACCCCCCC AAAAAAAA	7
AGA GCT ATT CCT TTC ACT GCT ACA GTG CAT CCT TAT GCA ATT ACA GCT Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala 5 10 15	5
CCA AGG TTG GTG GTG AAA ATG TCA GCA ATA GCC ACC AAG AAT ACA AGA Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg 20 25 30	3
GTG GAG TCA TTA GAG GTG AAA CCA CCA GCA CAC CCA ACT TAT GAT TTA Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu 35 40 45 50	1
AAG GAA GTT ATG AAA CTT GCA CTC TCT GAA GAT GCT GGG AAT TTA GGA Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly 55 60 65	9
GAT GTG ACT TGT AAG GCG ACA ATT CCT. CTT GAT ATG GAA TCC GAT GCT Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala 70 75 80	7
CAT TTT CTA GCA AAG GAA GAC GGG ATC ATA GCA GGA ATT GCA CTT GCT His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala 85 90 95	5
GAG ATG ATA TTC GCG GAA GTT GAT CCT TCA TTA AAG GTG GAG TGG TAT Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr 100 105	3
GTA AAT GAT GGC GAT AAA GTT CAT AAA GGC TTG AAA TTT GGC AAA GTA Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val 115 120 125 130	1
CAA GGA AAC GCT TAC AAC ATT GTT ATA GCT GAG AGG GTT GTT CTC AAT Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn 135 140 145	9
TTT ATG CAA AGA ATG AGT GGA ATA GCT ACA CTA ACT AAG GAA ATG GCA Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala 150 155 160	7
GAT GCT GCA CAC CCT GCT TAC ATC TTG GAG ACT AGG AAA ACT GCT CCT Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro 165 170 175	5

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GGA TTA CGT TTG GTG GAT AAA TGG GCG GTA TTG ATC GGT GGG GGG AAG Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys 180 185	633
AAT CAC AGA ATG GGC TTA TTT GAT ATG GTA ATG ATA AAA GAC AAT CAC Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His 200 205 210	681
ATA TCT GCT GCA GGT GTC GGC AAA GCT CTA AAA TCT GTG GAT CAG Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln 215 220 225	729
TAT TTG GAG CAA AAT AAA CTT CAA ATA GGG GTT GAG GTT GAA ACC AGG Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg 230 235 240	777
ACA ATT GAA GAA GTA CGT GAG GTT CTA GAC TAT GCA TCT CAA ACA AAG Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys 245 250 255	825
ACT TCG TTG ACT AGG ATA ATG CTG GAC AAT ATG GTT GTT CCA TTA TCT Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser 260 . 270	873
AAC GGA GAT ATT GAT GTA TCC ATG CTT AAG GAG GCT GTA GAA TTG ATC Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile 275 280 285 290	921
AAT GGG AGG TTT GAT ACG GAG GCT TCA GGA AAT GTT ACC CTT GAA ACA Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr 295 300 305	969
GTA CAC AAG ATT GGA CAA ACT GGT GTT ACC TAC ATT TCT AGT GGT GCC Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala 310 315 320	1017
CTG ACG CAT TCC GTG AAA GCA CTT GAC ATT TCC CTG AAG ATC GAT ACA Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr 325 330 335	1065
GAG CTC GCC CTT GAA GTT GGA AGG CGT ACA AAA CGA GCA TGAGCGCCAT Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala 340 345 350	1114
TACTTCTGCT ATAGGGTTGG AGTAAAAGCA GCTGAATAGC TGAAAGGTGC AAATAAGAAT	1174
CATTTTACTA GTTGTCAAAC AAAAGATCCT TCACTGTGTA ATCAAACAAA AAGATGTAAA	1234
TTGCTGGAAT ATCTCAGATG GCTCTTTTCC AACCTTATTG CTTGAGTTGG TAATTTCATT	1294
ATAGCTTTGT TTTCATGTTT CATGGAATTT GTTACAATGA AAATACTTGA TTTATAAGTT	1354
TGGTGTATGT AAAATTCTGT GTTACTTCAA ATATTTTGAG ATGTT	1399

- (2) INFORMATION FOR SEQ ID NO:2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Phe Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile 1 5 10 15

Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn 20 25 30

Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr 35 40 45

Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn 50 60

Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser 65 70 75 80

Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala 85 90 95

Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu 100 105 110

Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly 115 120

Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val 130 140

Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu 145 150 155 160

Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr 165 170 175

Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly 180 185 190

Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp 195 200 205

Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val 210 215 220

Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu 225 230 235 240

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Thr	Arg	Thr	Ile	G1u 245	Glu	Val	Arg	Glu	Va1 250	Leu	Asp	Tyr	Ala	Ser 255	Gln
Thr	Lys	Thr	Ser 260	Leu	Thr	Arg	Ile	Met 265	Leu	Asp	Asn	Met	Val 270	Val	Pro
Leu	Ser	Asn 275	Gly	Asp	Ile	Asp	Va1 280	Ser	Met	Leu	Lys	G1u 285	Ala	Val	Glu
	290		Gly			295					300				
G1u 305	Thr	Val	His	Lys	Ile 310	Gly	Gln	Thr	Gly	Val 315	Thr	Tyr	Ile	Ser	Ser 320
Gly	Ala	Leu	Thr	His 325	Ser	Val	Lys	Ala	Leu 330	Asp	Ile	Ser	Leu	Lys 335	Ile
Asp	Thr	Glu	Leu 340	Ala	Leu	Glu	Val	Gly 345	Arg	Arg	Thr	Lys	Arg 350	Ala	

(2) INFORMATION FOR SEQ ID NO:3: '

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1053 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

60	AGCTCCAAGG	ATGCAATTAC	GTGCATCCTT	CACTGCTACA	CTATTCCTTT	ATGTTTAGAG
120	ATTAGAGGTG	GAGTGGAGTC	AAGAATACAA	AATAGCCACC	AAATGTCAGC	TTGGTGGTGA
180	ACTCTCTGAA	TGAAACTTGC	AAGGAAGTTA	TTATGATTTA	CACACCCAAC	AAACCACCAG
240	TATGGAATCC	TTCCTCTTGA	AAGGCGACAA	TGTGACTTGT	ATTTAGGAGA	GATGCTGGGA
300	TGCTGAGATG	GAATTGCACT	ATCATAGCAG	GGAAGACGGG	TTCTAGCAAA	GATGCTCATT
360	TGGCGATAAA	ATGTAAATGA	GTGGAGTGGT	TTCATTAAAG	AAGTTGATCC	ATATTCGCGG
420	TGTTATAGCT	CTTACAACAT	CAAGGAAACG	TGGCAAAGTA	GCTTGAAATT	GTTCATAAAG
480	AACTAAGGAA	TAGCTACACT	ATGAGTGGAA	TATGCAAAGA	TTCTCAATTT	GAGAGGGTTG
540	TCCTGGATTA	GGAAAACTGC	TTGGAGACTA	TGCTTACATC	CTGCACACCC	ATGGCAGATG
600	AATGGGCTTA	AGAATCACAG	GGTGGGGGGA	GGTATTGATC	ATAAATGGGC	CGTTTGGTGG